

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: March 14, 2003, 05:41:04 ; Search time 3219 Seconds
(without alignments)
2332.564 Million cell updates/sec

Title: US-09-698-781-3

Perfect score: 258
Sequence: 1 MKOILHPALETMTATLFPVL.....KHQLVRSCKASCNSNSIY 258

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 1

Total number of hits satisfying chosen parameters: 761465

Minimum DB seq length: 20
Maximum DB seq length: 99

Post-processing: Listing first 100 summaries

Command line parameters:

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-Db-GenEmbl -OFMT-fastest -SUFFIX-oli.rge -MINMATCH=0.1 -LOOPEXT=0
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41: em_higo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	2.7	41	6	AR198454
2	7	2.7	45	6	I42997
3	7	2.7	81	9	HSU55120
4	6	2.3	20	12	AB069418
5	6	2.3	22	6	BD001095
6	6	2.3	22	6	BD001524
7	6	2.3	24	6	AX444205
8	6	2.3	25	6	AR037955
9	6	2.3	25	6	AX448171
10	6	2.3	25	6	AX476421
11	6	2.3	25	6	AX476422
12	6	2.3	25	6	AX476423
13	6	2.3	25	6	AX476424
14	6	2.3	25	6	AX476425
15	6	2.3	25	6	AX476426
16	6	2.3	25	6	AX476427
17	6	2.3	25	6	AX476428
18	6	2.3	27	6	AR018050
19	6	2.3	27	6	AR071940
20	6	2.3	28	6	AR009658
21	6	2.3	28	6	AR053923
22	6	2.3	28	6	AR053924
23	6	2.3	28	6	I18678
24	6	2.3	28	6	I18679
25	6	2.3	30	6	AR145382
26	6	2.3	30	6	AX338650
27	6	2.3	30	6	AX356035
28	6	2.3	30	6	I36155
29	6	2.3	31	6	AX203821
30	6	2.3	31	6	AR110559
31	6	2.3	32	6	AR151779
32	6	2.3	32	6	AR182160
33	6	2.3	32	6	AX111383
34	6	2.3	39	6	AX111383
35	6	2.3	40	6	AR053703
36	6	2.3	43	6	I42996
37	6	2.3	43	6	AR021117
38	6	2.3	48	6	AR036261
39	6	2.3	49	6	AR120167
40	6	2.3	49	6	AR126165
41	6	2.3	49	6	AR177981
42	6	2.3	50	6	AR135508
43	6	2.3	50	6	AX156996
44	6	2.3	50	6	I21540
45	6	2.3	50	6	I21541
46	6	2.3	51	6	AX116773
47	6	2.3	51	6	AX118021
48	6	2.3	51	6	AX156995
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50	6	2.3	51	6	AX157428
51	6	2.3	51	6	AX157553

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53 2.3 51 6 AX157714 Sequence
54 2.3 51 6 AX161985 Sequence
55 2.3 51 6 AX161986 Sequence
56 2.3 51 6 AX203925 Sequence
57 2.3 51 6 AX204037 Sequence
58 2.3 52 6 AR209852 Sequence
59 2.3 52 6 AX107695 Sequence
60 2.3 53 6 EA3317 Composition
61 2.3 54 6 HSDPTNBVRC Y15721 Homo sapien
62 2.3 53 6 AR120176 Sequence
63 2.3 63 6 AR126174 Sequence
64 2.3 63 6 AR177990 Sequence
65 2.3 66 6 AR079745 Sequence
66 2.3 66 6 AR081275 Sequence
67 2.3 66 6 AR170635 Sequence
68 2.3 69 6 AR200610 Sequence
69 2.3 69 6 AX461658 Sequence
70 2.3 70 6 AR135261 Sequence
71 2.3 70 6 AR147236 Sequence
72 2.3 73 6 AX356671 Sequence
73 2.3 74 6 AX32391 Sequence
74 2.3 74 6 I56530 Sequence
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77 2.3 84 6 E03577 DNA sequence
78 2.3 85 6 E07901 DNA fragment
79 2.3 85 10 MUSIGNTCA M12568 Mouse unpro
80 2.3 85 10 MUSC4A14 M13026 Mouse alpha
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84 2.3 88 9 AY006103 AY006103 Homo sapi
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86 2.3 91 6 I73569 I73569 Sequence
87 2.3 92 3 TOXRSS1 M17555 T.gondii sm
88 2.3 96 4 BOVOST4 M18876 Cow osteone
89 2.3 96 9 HUMC5A2 M1135 Human proco
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92 2.3 98 10 MAZ86079 286079 M.auratus D
93 2.3 99 6 AX351035 AX351035 Sequence
94 1.9 20 6 DOGP39102 L24283 Dog (Clone:
95 1.9 20 6 AA8545 AA8545 Sequence
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98 1.9 20 6 AR016116 AR016116 Sequence
99 1.9 20 6 AR019114 AR019114 Sequence
100 1.9 20 6 AR054611 AR054611 Sequence

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ALIGNMENTS

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RESULT 1
LOCUS AR198454 41 bp DNA
DEFINITION Sequence 63 from patent US 6352851.
ACCESSION AR198454
VERSION AR198454.1 GI:20248303
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41)
AUTHORS Nielsen,B,Roenfeldt., Svendsen,A., Pedersen,H., Vind,J.,
Hendriksen,H,Vang. and Frandsen,T,Peter.
TITLE Glucosylase variants
JOURNAL Patent: US 6352851-A 63 05-MAR-2002;
FEATURES
Location/Qualifiers
source 1..41
7 a 11 c 11 g 12 t
BASE COUNT

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ORIGIN
Alignment Scores:
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Score: 7.00
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Best Local Similarity: 100.00%
Query Match: 2.71%
DB: 6
Gaps: 0

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US-09-698-781-3 (1-258) x AR198454 (1-41)

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QY 24 ValAlaGlyLeuLeuProSer 30
Db 4 GTGGCTGGACTTCTTCACAGC 24

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RESULT 2

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LOCUS 142997 45 bp DNA
DEFINITION Sequence 19 from patent US 5631115.
ACCESSION I42997
VERSION I42997.1 GI:2468241
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 45)
AUTHORS Ohtsuka,E. and Koizumi,M.
TITLE Looped, hairpin ribozyme
JOURNAL Patent: US 5631115-A 19 20-MAY-1997;
FEATURES
Location/Qualifiers
source 1..45
7 a 13 c 15 g 10 t
BASE COUNT
ORIGIN

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Alignment Scores:
Pred. No.: 105
Score: 7.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 2.71%
DB: 6
Gaps: 0

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US-09-698-781-3 (1-258) x I42997 (1-45)

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QY 63 ArgArgAlaValSerProPro 69
Db 2 CGACGGCGTGTTCGCCGCG 22

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RESULT 3

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LOCUS HS055120/c 81 bp mRNA
DEFINITION Human isolate HR051 T cell receptor V-beta complementarity
ACCESSION U55120
VERSION U55120.1 GI:1431965
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 81)
AUTHORS Li,Y., Uccelli,A., Laxer,K.D., Jeong,M.C., Vinters,H.V.,
Tourtellotte,W.W., Hauser,S.L. and Oksenberg,J.R.
TITLE Local clonal expansion of infiltrating T lymphocytes in chronic
encephalitis of Rasmussen
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 81)
AUTHORS Oksenberg,J.
TITLE Direct Submission
JOURNAL Submitted (16-Apr-1996) Jorge Oksenberg, Department of Neurology,
UCSF Medical Center, Box 0435, 3rd and Parnassus Avenues, San

```

Francisco, CA 94143, USA

FEATURES
source
1. 81
/organism="Homo sapiens"
/isolate="HR051"
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/tissue="brain"
/note="patient HR-4, sample B"
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/product="V cell receptor V-beta complementarity
determining region 3"
/protein_id="AAB03947.1"
/db_xref="GI:1431966"
/translation="TSVYFCALINGCYQEYFGPCTRLVT"
BASE COUNT 19 a 25 c 22 g 15 t
ORIGIN

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Pred. No.: 180 Length: 81
Score: 7.00 Matches: 7
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Best Local Similarity: 100.00% Indels: 0
Query Match: 2.71% Gaps: 0
DB: 9

US-09-698-781-3 (1-258) x HSUS5120 (1-81)
Oy 19 ValleuLeuPheluVala 25
Db 51 GTRCTGCTCTTCTGTGATGCC 31

RESULT 4
AB069418 20 bp DNA linear SYN 08-AUG-2001
LOCUS Synthetic construct DNA, forward primer for human STS sts-DIS2749
DEFINITION at 1p36.
ACCESSION AB069418
VERSION AB069418.1 GI:15130222
KEYWORDS synthetic construct DNA.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Chen, Y. Z., Hayashi, Y., Wu, J. G., Takaoka, E., Maekawa, K., Watanabe, N., Inazawa, J., Hosoda, F., Arai, Y., Mizushima, H., Morohashi, A., Ohlira, M., Nakagawara, A., Iiu, S., Hoshi, M., Horii, A. and Soda, E.
TITLE A BAC-based STS-content map spanning a 35-kb region of human
JOURNAL Chromosome 1p35-p36
MEDLINE 21269192
REFERENCE 2 (bases 1 to 20)
AUTHORS Horii, A.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2001) Akira Horii, Tohoku University School of Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-Ku, Sendai, Miyagi 980-8575, Japan (E-mail: horii@mail.cc.tohoku.ac.jp, Tel: 81-22-717-8042, Fax: 81-22-717-8047)
FEATURES
source
1. 20
/organism="synthetic construct"
/db_xref="taxon:32630"
misc_feature
1. 20
/note="forward primer for human STS sts-DIS2749 at 1p36
sts-DIS2749 obtained from clones B223H7, B344H11, B285H13,
B84D12, Human BAC library PCRT-11"
BASE COUNT 2 a 6 c 4 g 8 t
ORIGIN

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Pred. No.: 534 Length: 20
Score: 6.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.33% Indels: 0
DB: 12 Gaps: 0

US-09-698-781-3 (1-258) x AB069418 (1-20)
Oy 38 AsproAlaPhethAla 43
Db 1 GATCGCTTACTGCT 18

RESULT 5
BD001095 22 bp RNA linear PAT 31-JAN-2002
LOCUS Method and reagent for inhibiting viral replication.
DEFINITION BD001095
ACCESSION BD001095.1 GI:18626554
VERSION JP 2000342285-A/255.
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 22)
AUTHORS Draper, K.G., Dadyktz, L.W., Macswigen, J.A., Maysejak, D.G., Holesek, J.J. and Mamone, A.J.
TITLE Method and reagent for inhibiting viral replication
JOURNAL Patent: JP 2000342285-A 255 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
COMMENT PN JP 2000342285-A/255
PD 12-DEC-2000
PR 01-MAY-2000 JP 2000132616
PR 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882891 PR
14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/883873 PR
14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884521 PR
14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR
15-OCT-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER, LEC W DADYKTZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLESEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00, C12N9/22, C12N5/10, C12N1/91, PC
C12N15/00,
PC C12N5/00, C12N5/00, C12N1/91)
CC
FH Key Location/Qualifiers
FT source 1. 22
/organism="Artificial Sequence".
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1. 22
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 5 a 4 c 10 g 3 t
ORIGIN

Alignment Scores:
Pred. No.: 583 Length: 22
Score: 6.00 Matches: 6
Conservative: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 2.33% Gaps: 0
DB: 6

US-09-698-781-3 (1-258) x BD001095 (1-22)
Oy 116 SerSerAlaProSerSer 121


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LOCUS AX448171 25 bp DNA linear PAT 03-JUL-2002
DEFINITION Sequence 4626 from Patent WO0216649.
ACCESSION AX448171
VERSION AX448171.1 GI:21697070
KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequences.
REFERENCE
1 Gunderson,K.
AUTHORS Probes and decoder oligonucleotides
TITLE Patent: WO 0216649-A 4626 28-FEB-2002;
JOURNAL Illumina, Inc. (US)
FEATURES
source 1..25
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
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ORIGIN

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Pred. No.: 655 Length: 25
Score: 6.00 Matches: 6
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.33% Indels: 0
DB: 6 Gaps: 0

US-09-698-781-3 (1-258) x AX448171 (1-25)

QY 203 ProCysAlaSerCysPro 208
Db 6 CCGTCGCTTCATGTCCT 23

RESULT 10
AX476421 25 bp DNA linear PAT 12-AUG-2002
LOCUS AX476421
DEFINITION Sequence 1642 from Patent WO0224750.
ACCESSION AX476421
VERSION AX476421.1 GI:22215706
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Zhang,J.
AUTHORS Human kidney tumor overexpressed membrane protein 1
TITLE Patent: WO 0224750-A 1642 28-MAR-2002;
JOURNAL Aeomica, Inc. (US)
FEATURES
source 1..25
Location/Qualifiers
/organism="Homo sapiens"
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BASE COUNT 3 a 9 c 5 g 8 t
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Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.33% Indels: 0
DB: 6 Gaps: 0

US-09-698-781-3 (1-258) x AX476421 (1-25)

QY 202 AlaProCysAlaSerCys 207
Db 8 GCTCCCTGCGCCTTGT 25

RESULT 11
AX476422 25 bp DNA linear PAT 12-AUG-2002
LOCUS AX476422
DEFINITION Sequence 1643 from Patent WO0224750.
ACCESSION AX476422
VERSION AX476422.1 GI:22215707
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Zhang,J.
AUTHORS Human kidney tumor overexpressed membrane protein 1
TITLE Patent: WO 0224750-A 1643 28-MAR-2002;
JOURNAL Aeomica, Inc. (US)
FEATURES
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Location/Qualifiers
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BASE COUNT 3 a 10 c 5 g 7 t
ORIGIN

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Pred. No.: 655 Length: 25
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.33% Indels: 0
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US-09-698-781-3 (1-258) x AX476422 (1-25)

QY 202 AlaProCysAlaSerCys 207
Db 7 GCTCCCTGCGCCTTGT 24

RESULT 12
AX476423 25 bp DNA linear PAT 12-AUG-2002
LOCUS AX476423
DEFINITION Sequence 1644 from Patent WO0224750.
ACCESSION AX476423
VERSION AX476423.1 GI:22215708
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Zhang,J.
AUTHORS Human kidney tumor overexpressed membrane protein 1
TITLE Patent: WO 0224750-A 1644 28-MAR-2002;
JOURNAL Aeomica, Inc. (US)
FEATURES
source 1..25
Location/Qualifiers
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Score: 6.00 Matches: 6
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Best Local Similarity: 100.00% Mismatches: 0
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DB: 6 Gaps: 0

US-09-698-781-3 (1-258) x AX476423 (1-25)
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AX476424
LOCUS AX476424 25 bp DNA Linear PAT 12-AUG-2002
DEFINITION Sequence 1645 from Patent WO0224750.
ACCESSION AX476424
VERSION AX476424.1 GI:22215709
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Zhang, J.
AUTHORS Human kidney tumor overexpressed membrane protein 1
TITLE Patent: WO 0224750-A 1645 28-MAR-2002;
JOURNAL Aecomica, Inc. (US)
FEATURES
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BASE COUNT 3 a 10 c 6 g 6 t
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.33% Indels: 0
Gaps: 0
DB: 0
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OY 202 AlaprocysAlaserCys 207
Db 5 GCTCCCTGGCCTCTGT 22
RESULT 14
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LOCUS AX476425 25 bp DNA Linear PAT 12-AUG-2002
DEFINITION Sequence 1646 from Patent WO0224750.
ACCESSION AX476425
VERSION AX476425.1 GI:22215710
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Zhang, J.
AUTHORS Human kidney tumor overexpressed membrane protein 1
TITLE Patent: WO 0224750-A 1646 28-MAR-2002;
JOURNAL Aecomica, Inc. (US)
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RESULT 15
AX476426
LOCUS AX476426 25 bp DNA Linear PAT 12-AUG-2002
DEFINITION Sequence 1647 from Patent WO0224750.
ACCESSION AX476426
VERSION AX476426.1 GI:22215711
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Zhang, J.
AUTHORS Human kidney tumor overexpressed membrane protein 1
TITLE Patent: WO 0224750-A 1647 28-MAR-2002;
JOURNAL Aecomica, Inc. (US)
FEATURES
source Location/Qualifiers
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Db 3 GCTCCCTGGCCTCTGT 20
RESULT 16
AX476427
LOCUS AX476427 25 bp DNA Linear PAT 12-AUG-2002
DEFINITION Sequence 1648 from Patent WO0224750.
ACCESSION AX476427
VERSION AX476427.1 GI:22215712
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Zhang, J.
AUTHORS Human kidney tumor overexpressed membrane protein 1
TITLE Patent: WO 0224750-A 1648 28-MAR-2002;
JOURNAL Aecomica, Inc. (US)
FEATURES
source Location/Qualifiers
1..25
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 2 a 11 c 5 g 7 t
ORIGIN
Alignment Scores:
Pred. No.: 655 Length: 25
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.33% Indels: 0
Gaps: 0
DB: 0
US-09-698-781-3 (1-258) x AX476427 (1-25)
OY 202 AlaprocysAlaserCys 207
Db 11 GCTCCCTGGCCTCTGT 21
```

Db 2 GCTCCTCGCGCTCTTGT 19

RESULT 17

AX476428

LOCUS

DEFINITION Sequence 1649 from Patent WO0224750.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-698-781-3 (1-258) x AX476428 (1-25)

OY 202 Alaprocysalasecys 207

Db 1 GCTCCTCGCGCTCTTGT 18

RESULT 18

AR018050/c

LOCUS

DEFINITION Sequence 7 from patent US 5780386.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-698-781-3 (1-258) x AR018050 (1-27)

OY 42 ThAlaleuleuthrthr 47

Db 20 ACAGCTCTGCTAACAC 3

RESULT 19

AR071940/c

LOCUS

DEFINITION Sequence 7 from patent US 5912159.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-698-781-3 (1-258) x AR071940 (1-27)

OY 62 leuargalavalser 67

Db 28 CTGCGGCGAGCGGTATCA 11

RESULT 20

AR009658/c

LOCUS

DEFINITION Sequence 12 from patent US 5756334.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-698-781-3 (1-258) x AR009658 (1-28)

OY 62 leuargalavalser 67

Db 28 CTGCGGCGAGCGGTATCA 11

RESULT 21

AR053923/c

LOCUS

DEFINITION Sequence 10 from patent US 5834285.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-698-781-3 (1-258) x AR053923 (1-28)

OY 62 leuargalavalser 67

Db 28 CTGCGGCGAGCGGTATCA 11

RESULT 22

AR053923/c

LOCUS

DEFINITION Sequence 10 from patent US 5834285.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-698-781-3 (1-258) x AR053923 (1-28)

OY 62 leuargalavalser 67

Db 28 CTGCGGCGAGCGGTATCA 11

```

ACCESSION   AR053923
VERSION     AR053923.1  GI:5978785
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 28)
AUTHORS    Comb,D.G., Perler,F., Kucera,R. and Jack,W.E.
TITLE      Recombinant thermostable DNA polymerase from archaeobacteria
JOURNAL    Patent: US 5834285-A 10 10-NOV-1998;
FEATURES
source      1..28
            /organism="unknown"
BASE COUNT  5 a 8 c 9 g 6 t
ORIGIN
Alignment Scores:
Pred. No.: 727      Length: 28
Score: 6.00      Matches: 6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.33%      Indels: 0
DB: 6      Gaps: 0

US-09-698-781-3 (1-258) x AR053923 (1-28)

QY 62 LeuArgArgAlaValser 67
DB 28 CTGCGCGAGCGGTATCA 11

RESULT 22
AR053924
LOCUS      AR053924 28 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 11 from patent US 5834285.
ACCESSION  AR053924
VERSION     AR053924.1  GI:5978786
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 28)
AUTHORS    Comb,D.G., Perler,F., Kucera,R. and Jack,W.E.
TITLE      Recombinant thermostable DNA polymerase from archaeobacteria
JOURNAL    Patent: US 5834285-A 11 10-NOV-1998;
FEATURES
source      1..28
            /organism="unknown"
BASE COUNT  6 a 9 c 8 g 5 t
ORIGIN
Alignment Scores:
Pred. No.: 727      Length: 28
Score: 6.00      Matches: 6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.33%      Indels: 0
DB: 6      Gaps: 0

US-09-698-781-3 (1-258) x AR053924 (1-28)

QY 62 LeuArgArgAlaValser 67
DB 1 CTGCGCGAGCGGTATCA 18

RESULT 23
AR053924
LOCUS      AR053924 28 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 10 from patent US 5500363.
ACCESSION  AR053924
VERSION     AR053924.1  GI:1599033
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.

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REFERENCE   1 (bases 1 to 28)
AUTHORS    Comb,D.G., Perler,F., Kucera,R. and Jack,W.E.
TITLE      Recombinant thermostable DNA polymerase from archaeobacteria
JOURNAL    Patent: US 5500363-A 10 19-MAR-1996;
FEATURES
source      1..28
            /organism="unknown"
BASE COUNT  5 a 8 c 9 g 6 t
ORIGIN
Alignment Scores:
Pred. No.: 727      Length: 28
Score: 6.00      Matches: 6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.33%      Indels: 0
DB: 6      Gaps: 0

US-09-698-781-3 (1-258) x 118678 (1-28)

QY 62 LeuArgArgAlaValser 67
DB 28 CTGCGCGAGCGGTATCA 11

RESULT 24
AR053924
LOCUS      AR053924 28 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 11 from patent US 5500363.
ACCESSION  AR053924
VERSION     AR053924.1  GI:1599034
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 28)
AUTHORS    Comb,D.G., Perler,F., Kucera,R. and Jack,W.E.
TITLE      Recombinant thermostable DNA polymerase from archaeobacteria
JOURNAL    Patent: US 5500363-A 11 19-MAR-1996;
FEATURES
source      1..28
            /organism="unknown"
BASE COUNT  6 a 9 c 8 g 5 t
ORIGIN
Alignment Scores:
Pred. No.: 727      Length: 28
Score: 6.00      Matches: 6
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 2.33%      Indels: 0
DB: 6      Gaps: 0

US-09-698-781-3 (1-258) x 118679 (1-28)

QY 62 LeuArgArgAlaValser 67
DB 1 CTGCGCGAGCGGTATCA 18

RESULT 25
AR053924
LOCUS      AR053924 30 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6211430.
ACCESSION  AR053924
VERSION     AR053924.1  GI:15107249
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 30)
AUTHORS    John,M.E.
TITLE      Folate Promoter
JOURNAL    Patent: US 6211430-A 6 03-APR-2001;

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FEATURES (US) Location/Qualifiers
source 1..30
/organism="unknown"
/db_xref="taxon:32630"
/note="primer"
BASE COUNT 5 a 9 c 11 g 5 t
ORIGIN

Alignment Scores:
Pred. No.: 775 Length: 30
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.33% Indels: 0
Gaps: 0
DB: 0

US-09-698-781-3 (1-258) x ARI45382 (1-30)

QY 66 ValserProProAlaArg 71
Db 28 GTGAGTCACACAGCTCGA 11

RESULT 26
LOCUS AX338660 30 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 25 from Patent WO0164713.
ACCESSION AX338660
VERSION AX338660.1 GI:18129024
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Gasche, C., Zakeri, S. M. and Reinisch, W.
TITLE Mammalian interleukin-10 (IL-10) receptor variants
JOURNAL Patent: WO 0164713-A 25 07-SEP-2001;
FEATURES
source 1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="cDNA"
BASE COUNT 5 a 9 c 12 g 4 t
ORIGIN

Alignment Scores:
Pred. No.: 775 Length: 30
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.33% Indels: 0
Gaps: 0
DB: 0

US-09-698-781-3 (1-258) x AX338660 (1-30)

QY 200 GlnGlyAlaProCysAla 205
Db 11 CAGGAGAGCCCCCTGTCT 28

RESULT 27
LOCUS AX356035 30 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 6 from Patent WO0183729.
ACCESSION AX356035
VERSION AX356035.1 GI:18620597
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Nemerow, G. R., von Seggern, D. J. and Friedlander, M.
TITLE Vectors for ocular transduction and use thereof for genetic therapy
JOURNAL Patent: WO 0183729-A 6 08-NOV-2001;
Novartis AG (CH); The Scripps Research Institute (US); Nemerow,
Glen R. (US); Von Seggern, Daniel J. (US); Friedlander, Marty

FEATURES (US) Location/Qualifiers
source 1..30
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"
BASE COUNT 4 a 9 c 7 g 10 t
ORIGIN

Alignment Scores:
Pred. No.: 775 Length: 30
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.33% Indels: 0
Gaps: 0
DB: 0

US-09-698-781-3 (1-258) x AX356035 (1-30)

QY 79 AsnLysGluAlaAlaAla 84
Db 23 AATAAGAGAGCGCCGCG 6

RESULT 28
LOCUS I36155 30 bp DNA linear PAT 13-MAY-1997
DEFINITION Sequence 39 from patent US 5604131.
ACCESSION I36155
VERSION I36155.1 GI:2087379
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 30)
AUTHORS Wadsworth, S., Snyder, B., Reddy, V. B. and Wei, C.
TITLE cDNA-genomic DNA hybrid sequence encoding APP770 containing a
JOURNAL Patent: US 5604131-A 39 18-FEB-1997;
FEATURES
source 1..30
/organism="unknown"
BASE COUNT 11 a 7 c 9 g 3 t
ORIGIN

Alignment Scores:
Pred. No.: 775 Length: 30
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.33% Indels: 0
Gaps: 0
DB: 0

US-09-698-781-3 (1-258) x I36155 (1-30)

QY 26 GlyLeuLeuProSerPhe 31
Db 20 GGACTCTTACCTCGTTT 3

RESULT 29
LOCUS AX203821 31 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 80 from Patent WO0146698.
ACCESSION AX203821
VERSION AX203821.1 GI:15393265
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1
AUTHORS Schall, T. J., Talbot, D., Miao, Z. and Wei, Z.
TITLE Tethered ligands and methods of use
JOURNAL Patent: WO 0146698-A 80 28-JUN-2001;
Chemocentryx, Inc. (US)

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FEATURES             Location/Qualifiers
     source            1..31
                        /organism="synthetic construct"
                        /db_xref="taxon:32630"
                        /note="MRP-1 reverse primer"
BASE COUNT            8 a      7 c      7 g      9 t
ORIGIN

Alignment Scores:
Pred. No.:            799          Length:          31
Score:                6.00          Matches:          6
Percent Similarity:   100.00%       Conservative:    0
Best Local Similarity: 100.00%       Mismatches:     0
Query Match:         2.33%          Indels:         0
DB:                  6              Gaps:            0

US-09-698-781-3 (1-258) x AX203821 (1-31)

QY    13 AlameThrLeuphePro 18
      |||||
Db    11 GCATGCACCTGTGCCCA 28

RESULT 30
ARI10559
LOCUS   ARI10559          32 bp      DNA          linear      PAT 14-FEB-2001
DEFINITION Sequence 39 from patent US 6114601.
ACCESSION ARI10559
VERSION   ARI10559.1  GI:12826835
KEYWORDS
SOURCE    Unknown.
          ORGANISM      Unknown.
          UNCLASSIFIED.
REFERENCE 1 (bases 1 to 32)
AUTHORS   Kikuchi,Y., Kiyokawa,S., Shimada,Y., Ohbayashi,M., Shimada,R. and
          Okinaka,Y.
          TITLE        Plant genes encoding flavonoid-3', 5'-hydroxylase
          JOURNAL       Patent: US 6114601-A 39 05-SEP-2000;
          FEATURES      Location/Qualifiers
                        source            1..32
                        BASE COUNT        5 a      11 c      9 g      5 t      2 others
                        ORIGIN

Alignment Scores:
Pred. No.:            822          Length:          32
Score:                6.00          Matches:          6
Percent Similarity:   100.00%       Conservative:    0
Best Local Similarity: 100.00%       Mismatches:     0
Query Match:         2.33%          Indels:         0
DB:                  6              Gaps:            0

US-09-698-781-3 (1-258) x ARI10559 (1-32)

QY    138 PheGlyValGlyProLys 143
      |||||
Db    4  TTCGGAGTCGGCCCAAA 21

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Search completed: March 14, 2003, 06:43:47
 Job time : 3225 secs